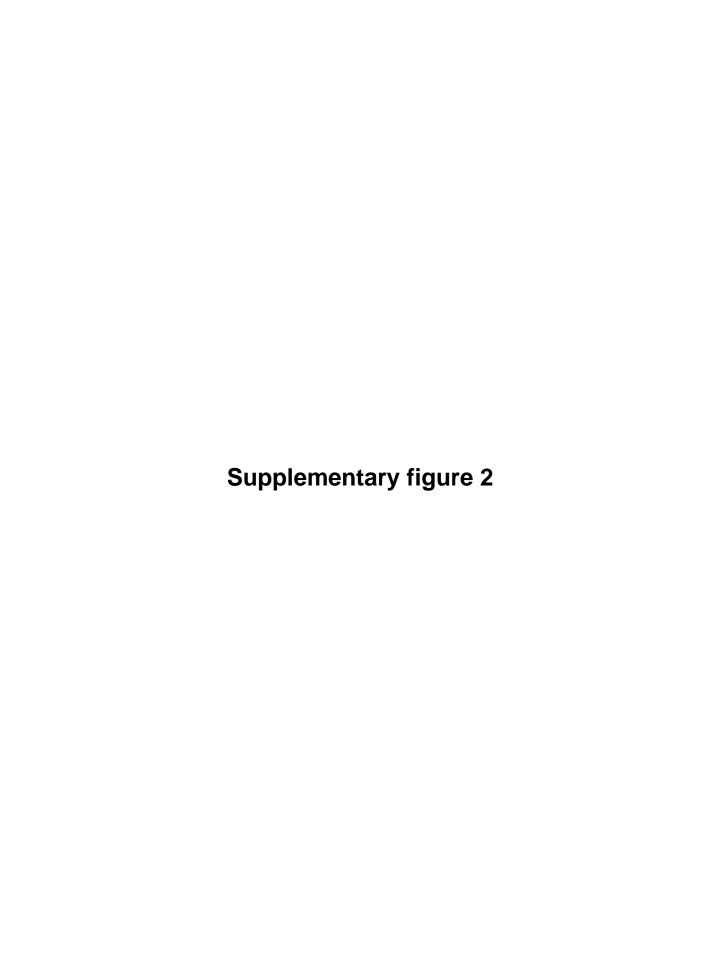


#### Supplementary figure 1: Replicate analysis

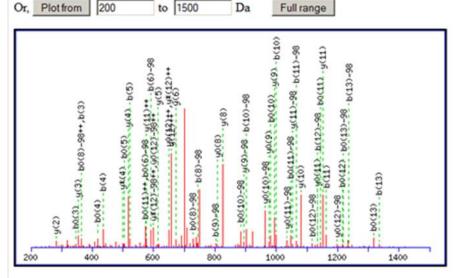
48 2DE spots were analysed in two biological replicates. 67 have been quantified and compared. The H/L ratios of the 2DE gel with 816 analyzed spots is shown in red and of the 2DE gel with 48 analyzed spots is shown in blue.



## Spot 75, phosphoserine

Data file C:\Mgf\_Mascot Daemon\HRP\VIME\HRP\_\_090512\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_75.mgf

Click mouse within plot area to zoom in by factor of two about that point



Monoisotopic mass of neutral peptide Mr(calc): 1513.69

Variable modifications:

S6 : Phospho (ST), with neutral losses 97.98(shown in table), 0.00

R14 : \_Label:13C(6) (R)
Ions Score: 50 Expect: 0.00043

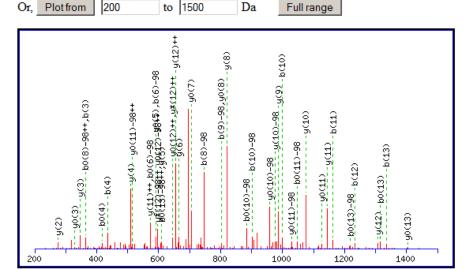
Matches (Bold Red): 52/190 fragment ions using 94 most intense peaks

#	b	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	у	y <sup>++</sup>	y*	y***	y <sup>0</sup>	y <sup>0++</sup>	#
1	88.04	44.52	70.03	35.52	S							14
2	201.12	101.07	183.11	92.06	L	1329.69	665.35	1312.66	656.84	1311.68	656.34	13
3	364.19	182.60	346.18	173.59	Y	1216.61	608.81	1199.58	600.29	1198.59	599.80	12
4	435.22	218.12	417.21	209.11	A	1053.54	527.27	1036.52	518.76	1035.53	518.27	11
5	522.26	261.63	504.25	252.63	S	982.50	491.76	965.48	483.24	964.49	482.75	10
6	591.28	296.14	573,27	287.14	S	895.47	448.24	878.45	439.73	877.46	439.23	9
7	688.33	344.67	670.32	335.66	P	826.45	413.73	809.42	405.22	808.44	404.72	8
8	745.35	373.18	727.34	364.17	G	729.40	365.20	712.37	356.69	711.39	356.20	7
9	802.37	401.69	784.36	392.68	G	672.38	336.69	655.35	328.18	654.37	327.69	6
10	901.44	451.22	883.43	442.22	v	615.36	308.18	598.33	299.67	597.35	299.18	5
11	1064.50	532.76	1046.49	523.75	Y	516.29	258.65	499.26	250.13	498.28	249.64	4
12	1135.54	568.27	1117.53	559.27	A	353.22	177.12	336.20	168.60	335.21	168.11	3
13	1236.59	618.80	1218.58	609.79	T	282.19	141.60	265.16	133.08	264.18	132.59	2
14					R	181.14	91.07	164.11	82.56			1

#### Spot 77, phosphoserine

Data file C:\Mgf\_Mascot Daemon\HRP\VIME\HRP\_\_090512\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_77.mgf

Click mouse within plot area to zoom in by factor of two about that point



Monoisotopic mass of neutral peptide Mr(calc): 1507.67

Variable modifications:

S6 : \_Phospho (ST), with neutral losses 0.00(shown in table), 97.98

Ions Score: 65 Expect: 1.4e-005

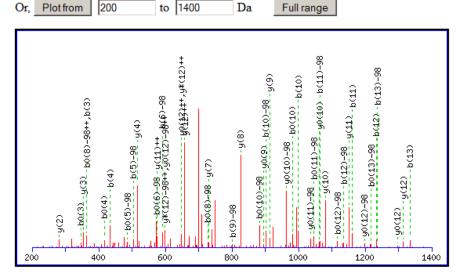
Matches (Bold Red): 44/190 fragment ions using 52 most intense peaks

#	b	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y****	y <sup>0</sup>	y <sup>0++</sup>	#
1	88.04	44.52	70.03	35.52	S							14
2	201.12	101.07	183.11	92.06	L	1421.65	711.33	1404.62	702.81	1403.64	702.32	13
3	364.19	182.60	346.18	173.59	Y	1308.56	654.78	1291.54	646.27	1290.55	645.78	12
4	435.22	218.12	417.21	209.11	A	1145.50	573.25	1128.47	564.74	1127.49	564.25	11
5	522.26	261.63	504.25	252.63	S	1074.46	537.73	1057.44	529.22	1056.45	528.73	10
6	689.25	345.13	671.24	336.13	S	987.43	494.22	970.40	485.71	969.42	485.21	9
7	786.31	393.66	768.30	384.65	P	820.43	410.72	803.40	402.21	802.42	401.71	8
8	843.33	422.17	825.32	413.16	G	723.38	362.19	706.35	353.68	705.37	353.19	7
9	900.35	450.68	882.34	441.67	G	666.36	333.68	649.33	325.17	648.35	324.68	6
10	999.42	500.21	981.41	491.21	V	609.34	305.17	592.31	296.66	591.32	296.17	5
11	1162.48	581.74	1144.47	572.74	Y	510.27	255.64	493.24	247.12	492.26	246.63	4
12	1233.52	617.26	1215.51	608.26	A	347.20	174.11	330.18	165.59	329.19	165.10	3
13	1334.57	667.79	1316.56	658.78	T	276.17	138.59	259.14	130.07	258.16	129.58	2
14					R	175.12	88.06	158.09	79.55			1

## Spot 77, phosphoserine

Data file C:\Mgf\_Mascot Daemon\HRP\VIME\HRP\_\_090512\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_77.mgf

Click mouse within plot area to zoom in by factor of two about that point



Monoisotopic mass of neutral peptide Mr(calc): 1513.69

Variable modifications:

S5 : Phospho (ST), with neutral losses 97.98(shown in table), 0.00

R14 : \_Label:13C(6) (R)

Ions Score: 61 Expect: 4.7e-005

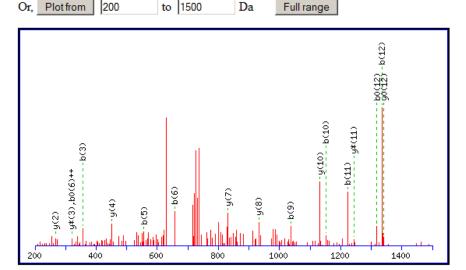
Matches (Bold Red): 45/188 fragment ions using 59 most intense peaks

#	b	b <sup>++</sup>	<b>b</b> <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y****	y <sup>0</sup>	y <sup>0++</sup>	#
1	88.04	44.52	70.03	35.52	S							14
2	201.12	101.07	183.11	92.06	L	1329.69	665.35	1312.66	656.84	1311.68	656.34	13
3	364.19	182.60	346.18	173.59	Y	1216.61	608.81	1199.58	600.29	1198.59	599.80	12
4	435.22	218.12	417.21	209.11	A	1053.54	527.27	1036.52	518.76	1035.53	518.27	11
5	504.25	252.63	486.23	243.62	S	982.50	491.76	965.48	483.24	964.49	482.75	10
6	591.28	296.14	573.27	287.14	S	913.48	457.25	896.46	448.73	895.47	448.24	9
7	688.33	344.67	670.32	335.66	P	826.45	413.73	809.42	405.22	808.44	404.72	8
8	745.35	373.18	727.34	364.17	G	729.40	365.20	712.37	356.69	711.39	356.20	7
9	802.37	401.69	784.36	392.68	G	672.38	336.69	655.35	328.18	654.37	327.69	6
10	901.44	451.22	883.43	442.22	V	615.36	308.18	598.33	299.67	597.35	299.18	5
11	1064.50	532.76	1046.49	523.75	Y	516.29	258.65	499.26	250.13	498.28	249.64	4
12	1135.54	568.27	1117.53	559.27	A	353.22	177.12	336.20	168.60	335.21	168.11	3
13	1236.59	618.80	1218.58	609.79	T	282.19	141.60	265.16	133.08	264.18	132.59	2
14					R	181.14	91.07	164.11	82.56			1

### Spot 77, cysteine trioxidation

Data file C:\Mgf\_Mascot Daemon\HRP\VIME\HRP\_\_090512\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_77.mgf

Click mouse within plot area to zoom in by factor of two about that point



Monoisotopic mass of neutral peptide Mr(calc): 1486.73

Variable modifications: C7 : Trioxidation (C) K13 : \_Label:13C(6) (K) Ions Score: 43 Expect: 0.0061

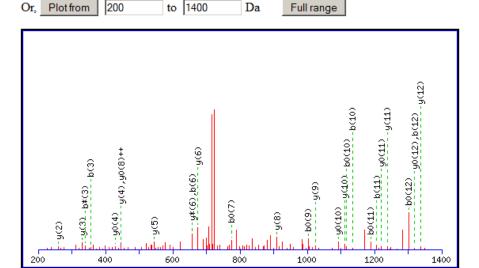
Matches (Bold Red): 17/132 fragment ions using 34 most intense peaks

#	b	b <sup>++</sup>	b*	b**++	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y***	y <sup>0</sup>	y <sup>0++</sup>	#
1	129.07	65.04	112.04	56.52			Q							13
2	228.13	114.57	211.11	106.06			V	1359.68	680.34	1342.65	671.83	1341.67	671.34	12
3	356.19	178.60	339.17	170.09			Q	1260.61	630.81	1243.58	622.29	1242.60	621.80	11
4	443.22	222.12	426.20	213.60	425.21	213.11	S	1132.55	566.78	1115.52	558.27	1114.54	557.77	10
5	556.31	278.66	539.28	270.14	538.30	269.65	L	1045.52	523.26	1028.49	514.75	1027.51	514.26	9
6	657.36	329.18	640.33	320.67	639.35	320.18	T	932.43	466.72	915.41	458.21	914.42	457.72	8
7	808.35	404.68	791.32	396.17	790.34	395.67	C	831.39	416.20	814.36	407.68	813.38	407.19	7
8	937.39	469.20	920.37	460.69	919.38	460.19	E	680.39	340.70	663.37	332.19	662.38	331.69	6
9	1036.46	518.73	1019.44	510.22	1018.45	509.73	V	551.35	276.18	534.32	267.67	533.34	267.17	5
10	1151.49	576.25	1134.46	567.73	1133.48	567.24	D	452.28	226.64	435.25	218.13	434.27	217.64	4
11	1222.53	611.77	1205.50	603.25	1204.52	602.76	A	337.25	169.13	320.23	160.62			3
12	1335.61	668.31	1318.58	659.80	1317.60	659.30	L	266.22	133.61	249.19	125.10			2
13							K	153.13	77.07	136.11	68.56			1

### Spot 78, cysteine dioxidation

Data file C:\Mgf\_Mascot Daemon\HRP\VIME\HRP\_\_090512\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_78.mgf

Click mouse within plot area to zoom in by factor of two about that point



Monoisotopic mass of neutral peptide Mr(calc): 1464.71

Variable modifications: C7 : Dioxidation (C)

Ions Score: 54 Expect: 0.00039

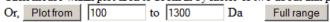
Matches (Bold Red): 27/132 fragment ions using 57 most intense peaks

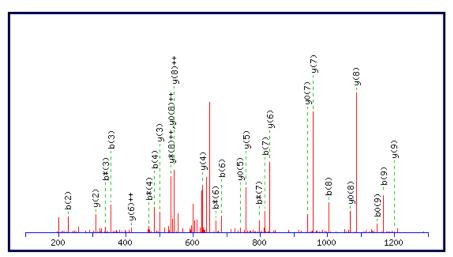
#	b	b <sup>++</sup>	b*	b**++	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y***	y <sup>0</sup>	y <sup>0++</sup>	#
1	129.07	65.04	112.04	56.52			Q							13
2	228.13	114.57	211.11	106.06			V	1337.66	669.33	1320.64	660.82	1319.65	660.33	12
3	356.19	178.60	339.17	170.09			Q	1238.59	619.80	1221.57	611.29	1220.58	610.80	11
4	443.22	222.12	426.20	213.60	425.21	213.11	S	1110.53	555.77	1093.51	547.26	1092.52	546.77	10
5	556.31	278.66	539.28	270.14	538.30	269.65	L	1023.50	512.25	1006.48	503.74	1005.49	503.25	9
6	657.36	329.18	640.33	320.67	639.35	320.18	T	910.42	455.71	893.39	447.20	892.41	446.71	8
7	792.36	396.68	775.33	388.17	774.35	387.68	C	809.37	405.19	792.34	396.68	791.36	396.18	7
8	921.40	461.20	904.37	452.69	903.39	452.20	E	674.37	337.69	657.35	329.18	656.36	328.68	6
9	1020.47	510.74	1003.44	502.22	1002.46	501.73	V	545.33	273.17	528.30	264.66	527.32	264.16	5
10	1135.49	568.25	1118.47	559.74	1117.48	559.25	D	446.26	223.63	429.23	215.12	428.25	214.63	4
11	1206.53	603.77	1189.50	595.26	1188.52	594.76	A	331.23	166.12	314.21	157.61			3
12	1319.61	660.31	1302.59	651.80	1301.60	651.31	L	260.20	130.60	243.17	122.09			2
13							K	147.11	74.06	130.09	65.55			1

### Spot 78, tryptophan kynurenin

Data file C:\Mgf\_Mascot Daemon\HRP\VIME\HRP\_\_090512\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_78.mgf

Click mouse within plot area to zoom in by factor of two about that point





Monoisotopic mass of neutral peptide Mr(calc): 1312.59

Variable modifications:

W8 : Trp->Kynurenin (W)
Ions Score: 67 Expect: 8.1e-006

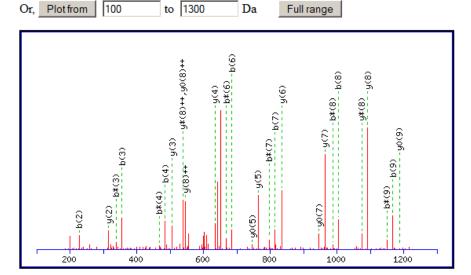
Matches (Bold Red): 27/96 fragment ions using 36 most intense peaks

#	b	b <sup>++</sup>	b*	b**++	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y***	y <sup>0</sup>	y <sup>0++</sup>	#
1	115.05	58.03	98.02	49.52			N							10
2	228.13	114.57	211.11	106.06			L	1199.56	600.28	1182.53	591.77	1181.55	591.28	9
3	356.19	178.60	339.17	170.09			Q	1086.47	543.74	1069.45	535.23	1068.46	534.74	8
4	485.24	243.12	468.21	234.61	467.22	234.12	E	958.42	479.71	941.39	471.20	940.40	470.71	7
5	556.27	278.64	539.25	270.13	538.26	269.63	A	829.37	415.19	812.35	406.68	811.36	406.18	6
6	685.32	343.16	668.29	334.65	667.30	334.16	E	758.34	379.67	741.31	371.16	740.32	370.67	5
7	814.36	407.68	797.33	399.17	796.35	398.68	E	629.29	315.15	612.27	306.64	611.28	306.14	4
8	1004.43	502.72	987.41	494.21	986.42	493.71	W	500.25	250.63	483.22	242.12			3
9	1167.50	584.25	1150.47	575.74	1149.48	575.25	Y	310.18	155.59	293.15	147.08			2
10							K	147.11	74.06	130.09	65.55			1

### Spot 78, tryptophan kynurenin

 $Data\ file\ C:\ \ Mgf\_Mascot\ Daemon\ \ HRP\ \ \_090512\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_78.mgf$ 

Click mouse within plot area to zoom in by factor of two about that point



Monoisotopic mass of neutral peptide Mr(calc): 1318.61

Variable modifications: W8 : Trp->Kynurenin (W) K10 : \_Label:13C(6) (K) Ions Score: 55 Expect: 0.00018

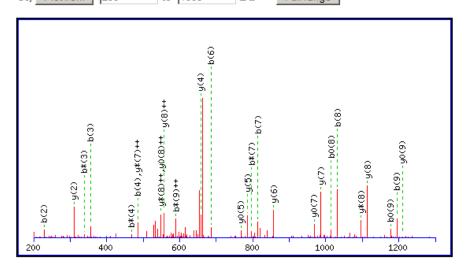
Matches (Bold Red): 27/96 fragment ions using 36 most intense peaks

#	b	b <sup>++</sup>	b*	b**++	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y*++	y <sup>0</sup>	y <sup>0++</sup>	#
1	115.05	58.03	98.02	49.52			N							10
2	228.13	114.57	211.11	106.06			L	1205.58	603.29	1188.55	594.78	1187.57	594.29	9
3	356.19	178.60	339.17	170.09			Q	1092.49	546.75	1075.47	538.24	1074.48	537.75	8
4	485.24	243.12	468.21	234.61	467.22	234.12	E	964.44	482.72	947.41	474.21	946.42	473.72	7
5	556.27	278.64	539.25	270.13	538.26	269.63	A	835.39	418.20	818.37	409.69	817.38	409.19	6
6	685.32	343.16	668.29	334.65	667.30	334.16	E	764.36	382.68	747.33	374.17	746.35	373.68	5
7	814.36	407.68	797.33	399.17	796.35	398.68	E	635.31	318.16	618.29	309.65	617.30	309.15	4
8	1004.43	502.72	987.41	494.21	986.42	493.71	W	506.27	253.64	489.24	245.13			3
9	1167.50	584.25	1150.47	575.74	1149.48	575.25	Y	316.20	158.60	299.17	150.09			2
10							K	153.13	77.07	136.11	68.56			1

### Spot 78, tryptophan formylkynurenin

Data file C:\Mgf Mascot Daemon\HRP\VIME\HRP 090512 HELA SILAC\_contr STLC 2DGE Jungblut Gel4\_78.mgf

Click mouse within plot area to zoom in by factor of two about that point Or, Plot from 200 to 1300 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1340.59

Variable modifications:

W8 : Trp->Formylkynurenin (W)
Ions Score: 50 Expect: 0.00041

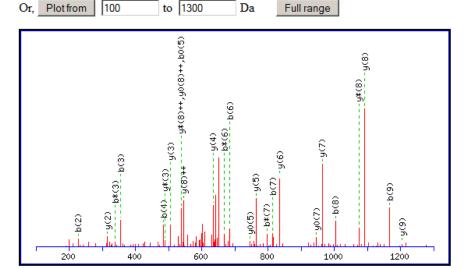
Matches (Bold Red): 27/96 fragment ions using 35 most intense peaks

#	b	b <sup>++</sup>	b*	b**++	<b>b</b> <sup>0</sup>	<b>b</b> <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y***	y <sup>0</sup>	y <sup>0++</sup>	#
1	115.05	58.03	98.02	49.52			N							10
2	228.13	114.57	211.11	106.06			L	1227.55	614.28	1210.53	605.77	1209.54	605.27	9
3	356.19	178.60	339.17	170.09			Q	1114.47	557.74	1097.44	549.22	1096.46	548.73	8
4	485.24	243.12	468.21	234.61	467.22	234.12	E	986.41	493.71	969.38	485.20	968.40	484.70	7
5	556.27	278.64	539.25	270.13	538.26	269.63	A	857.37	429.19	840.34	420.67	839.36	420.18	6
6	685.32	343.16	668.29	334.65	667.30	334.16	E	786.33	393.67	769.30	385.16	768.32	384.66	5
7	814.36	407.68	797.33	399.17	796.35	398.68	E	657.29	329.15	640.26	320.63	639.28	320.14	4
8	1032.43	516.72	1015.40	508.20	1014.42	507.71	W	528.25	264.63	511.22	256.11			3
9	1195.49	598.25	1178.46	589.74	1177.48	589.24	Y	310.18	155.59	293.15	147.08			2
10							K	147.11	74.06	130.09	65.55			1

# Spot 116, tryptophan kynurenin

Data file C:\Mgf\_Mascot Daemon\HRP\VIME\HRP\_090715\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_116.mgf

Click mouse within plot area to zoom in by factor of two about that point



Monoisotopic mass of neutral peptide Mr(calc): 1318.61

Variable modifications:

W8 : Trp->Kynurenin (W)
K10 : \_Label:13C(6) (K)
Ions Score: 61 Expect: 1.5e-005

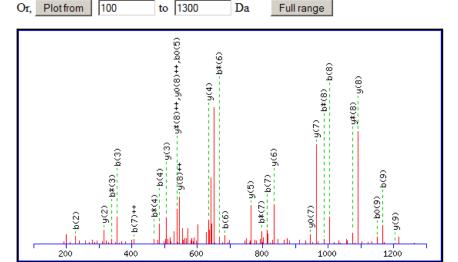
Matches (Bold Red): 26/96 fragment ions using 37 most intense peaks

#	b	b <sup>++</sup>	b*	b**++	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	<b>y</b> <sup>++</sup>	y*	y***	y <sup>0</sup>	y <sup>0++</sup>	#
1	115.05	58.03	98.02	49.52			N							10
2	228.13	114.57	211.11	106.06			L	1205.58	603.29	1188.55	594.78	1187.57	594.29	9
3	356.19	178.60	339.17	170.09			Q	1092.49	546.75	1075.47	538.24	1074.48	537.75	8
4	485.24	243.12	468.21	234.61	467.22	234.12	E	964.44	482.72	947.41	474.21	946.42	473.72	7
5	556.27	278.64	539.25	270.13	538.26	269.63	A	835.39	418.20	818.37	409.69	817.38	409.19	6
6	685.32	343.16	668.29	334.65	667.30	334.16	E	764.36	382.68	747.33	374.17	746.35	373.68	5
7	814.36	407.68	797.33	399.17	796.35	398.68	E	635.31	318.16	618.29	309.65	617.30	309.15	4
8	1004.43	502.72	987.41	494.21	986.42	493.71	W	506.27	253.64	489.24	245.13			3
9	1167.50	584.25	1150.47	575.74	1149.48	575.25	Y	316.20	158.60	299.17	150.09			2
10							K	153.13	77.07	136.11	68.56			1

### Spot 339, tryptophan kynurenin

Data file C:\Mgf\_Mascot Daemon\HRP\VIME\HRP\_\_091020\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_339.mgf

Click mouse within plot area to zoom in by factor of two about that point



Monoisotopic mass of neutral peptide Mr(calc): 1318.61

Variable modifications: W8 : Trp->Kynurenin (W) K10 : Label:13C(6) (K) Ions Score: 63 Expect: 3.1e-005

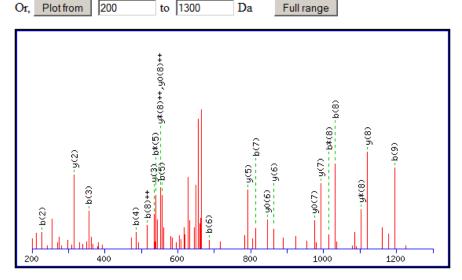
Matches (Bold Red): 28/96 fragment ions using 36 most intense peaks

#	b	b <sup>++</sup>	b*	b**++	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y***	y <sup>0</sup>	y <sup>0++</sup>	#
1	115.05	58.03	98.02	49.52			N							10
2	228.13	114.57	211.11	106.06			L	1205.58	603.29	1188.55	594.78	1187.57	594.29	9
3	356.19	178.60	339.17	170.09			Q	1092.49	546.75	1075.47	538.24	1074.48	537.75	8
4	485.24	243.12	468.21	234.61	467.22	234.12	E	964.44	482.72	947.41	474.21	946.42	473.72	7
5	556.27	278.64	539.25	270.13	538.26	269.63	A	835.39	418.20	818.37	409.69	817.38	409.19	6
6	685.32	343.16	668.29	334.65	667.30	334.16	E	764.36	382.68	747.33	374.17	746.35	373.68	5
7	814.36	407.68	797.33	399.17	796.35	398.68	E	635.31	318.16	618.29	309.65	617.30	309.15	4
8	1004.43	502.72	987.41	494.21	986.42	493.71	W	506.27	253.64	489.24	245.13			3
9	1167.50	584.25	1150.47	575.74	1149.48	575.25	Y	316.20	158.60	299.17	150.09			2
10							K	153.13	77.07	136.11	68.56			1

### Spot 355, tryptophan kynurenin

Data file C:\Mgf\_Mascot Daemon\HRP\VIME\HRP\_\_091020\_HELA\_SILAC\_contr\_STLC\_2DGE\_Jungblut\_Gel4\_355.mgf

Click mouse within plot area to zoom in by factor of two about that point



Monoisotopic mass of neutral peptide Mr(calc): 1346.61

Variable modifications:

W8 : Trp->Formylkynurenin (W)
K10 : \_Label:13C(6) (K)
Ions Score: 45 Expect: 0.00067

Matches (Bold Red): 22/96 fragment ions using 35 most intense peaks

#	b	b <sup>++</sup>	b*	b**++	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y***	y <sup>0</sup>	y <sup>0++</sup>	#
1	115.05	58.03	98.02	49.52			N							10
2	228.13	114.57	211.11	106.06			L	1233.57	617.29	1216.55	608.78	1215.56	608.28	9
3	356.19	178.60	339.17	170.09			Q	1120.49	560.75	1103.46	552.23	1102.48	551.74	8
4	485.24	243.12	468.21	234.61	467.22	234.12	E	992.43	496.72	975.40	488.21	974.42	487.71	7
5	556.27	278.64	539.25	270.13	538.26	269.63	A	863.39	432.20	846.36	423.68	845.38	423.19	6
6	685.32	343.16	668.29	334.65	667.30	334.16	E	792.35	396.68	775.32	388.17	774.34	387.67	5
7	814.36	407.68	797.33	399.17	796.35	398.68	E	663.31	332.16	646.28	323.64	645.30	323.15	4
8	1032.43	516.72	1015.40	508.20	1014.42	507.71	W	534.27	267.64	517.24	259.12			3
9	1195.49	598.25	1178.46	589.74	1177.48	589.24	Y	316.20	158.60	299.17	150.09			2
10							K	153.13	77.07	136.11	68.56			1